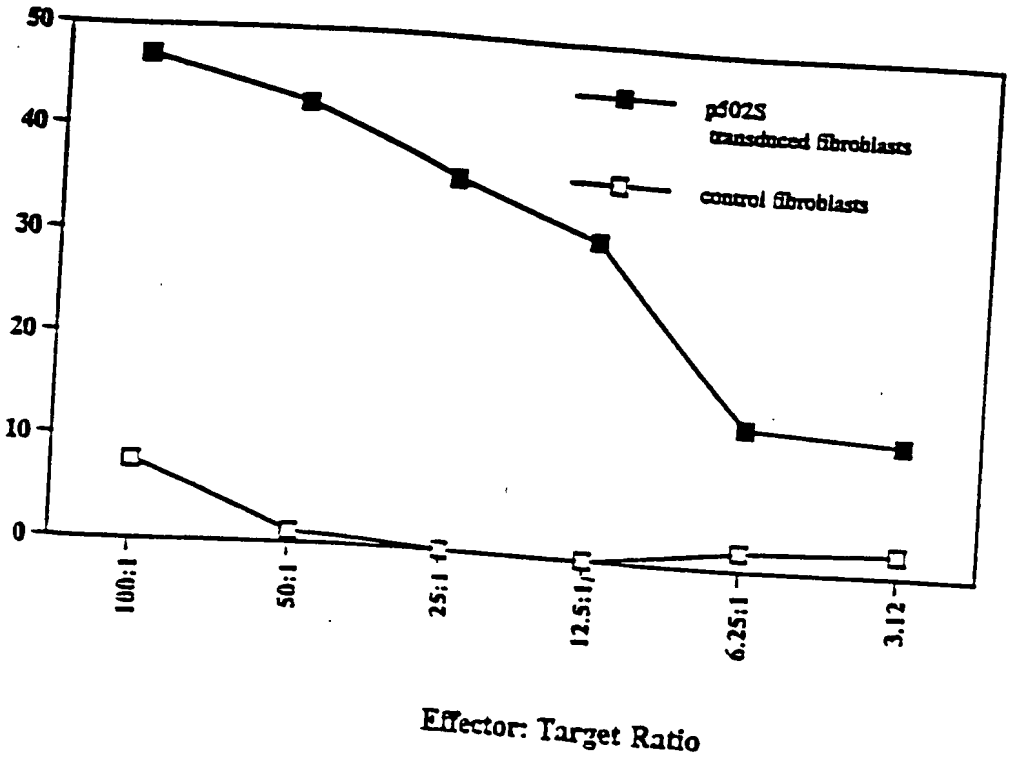

50
40
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

Document ID: US 2002/0164340 A1

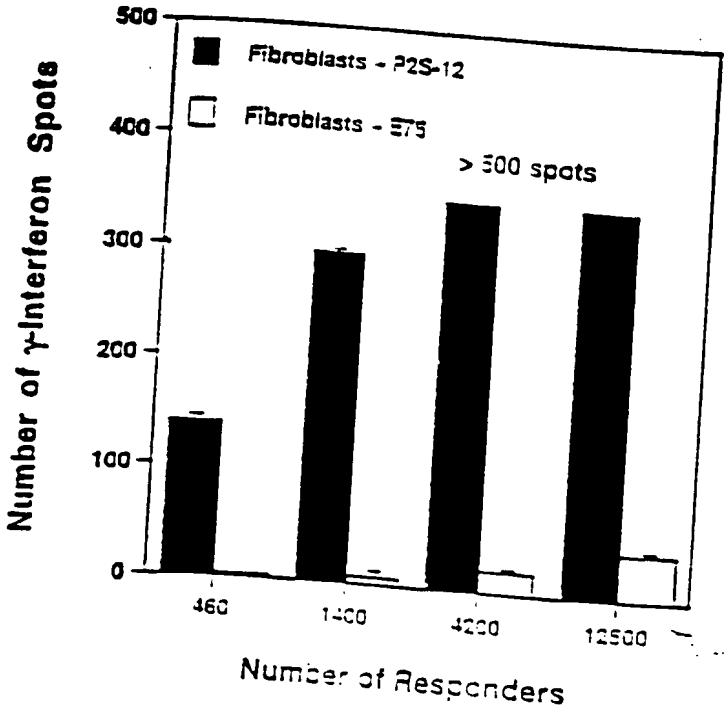


Fig. 2A

SUBSTITUTE SHEET (RULE 26)

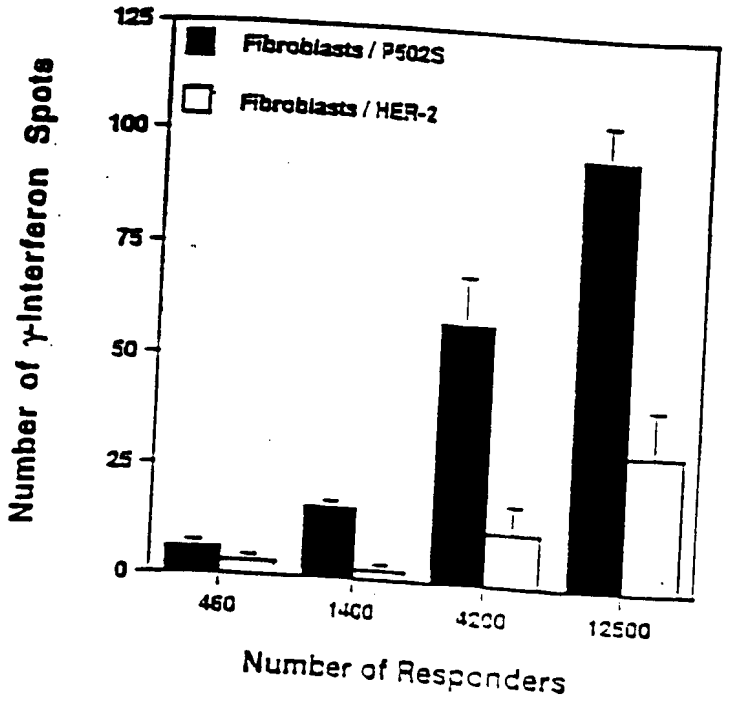


Fig. 2B

SUBSTITUTE SHEET (RULE 26)

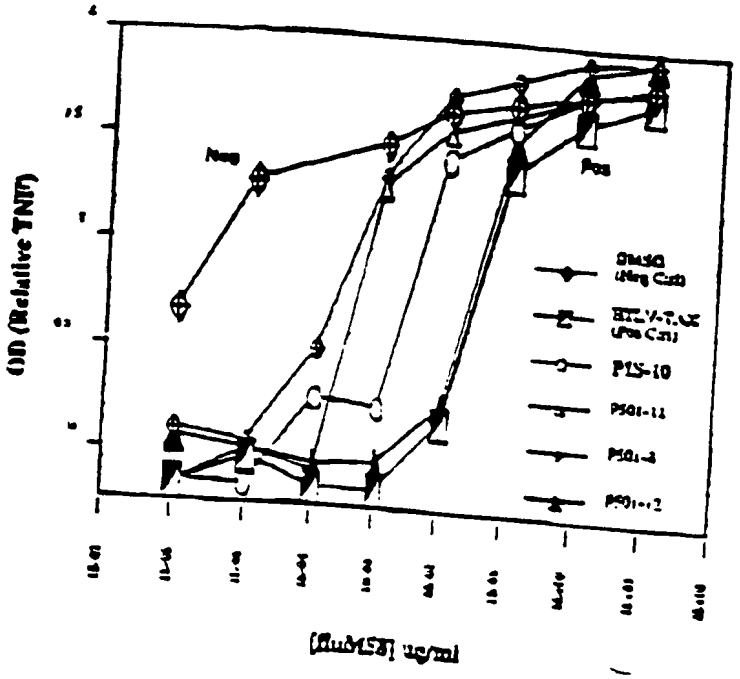


Fig. 3

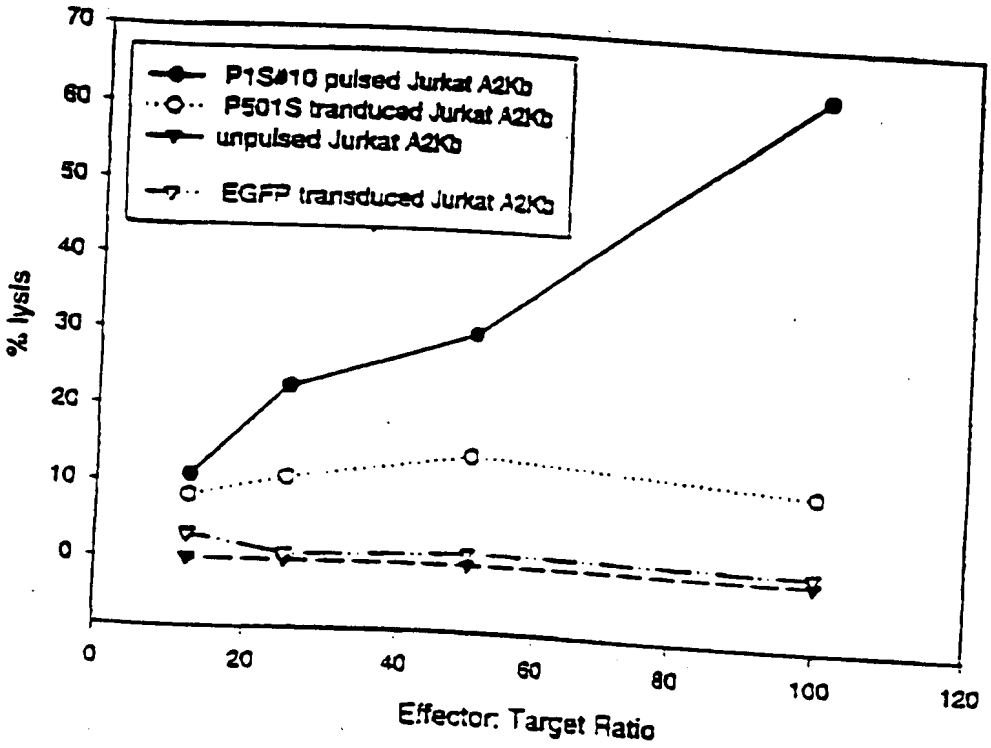

70
60
50
40
30
20
10
0
% lysis
P1S#10 pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
0
20
40
60
80
100
120
Effector: Target Ratio

Fig. 4

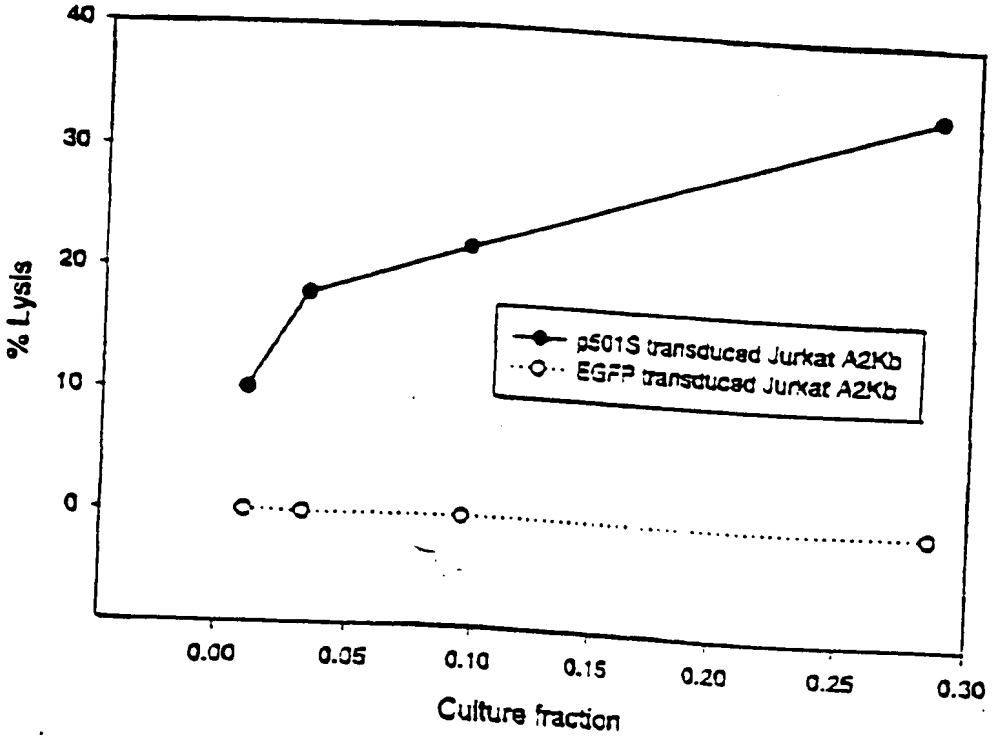

40
30
20
10
0
% Lysis
pS01S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Culture fraction

Fig. 5

66ETTT' ETE6Eh6O

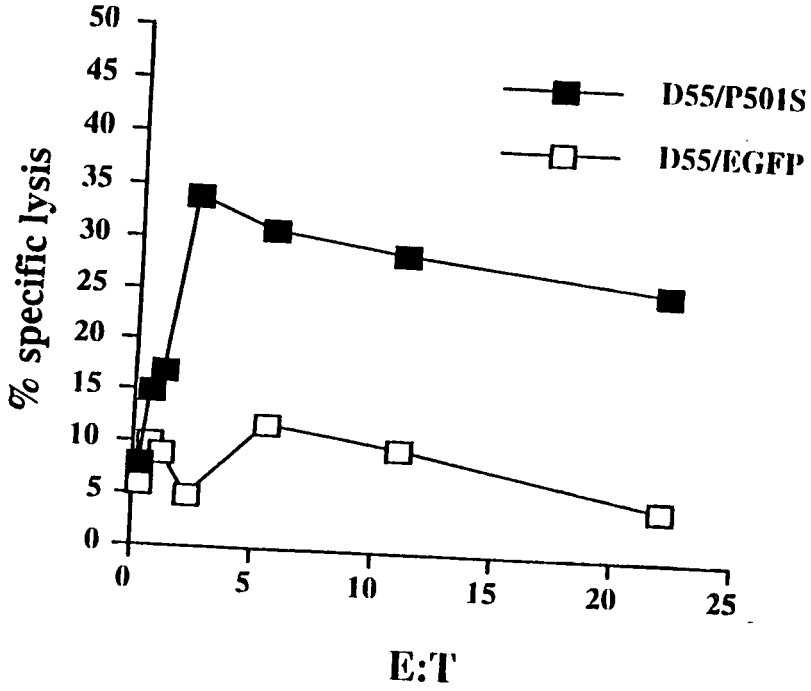


Fig. 6A

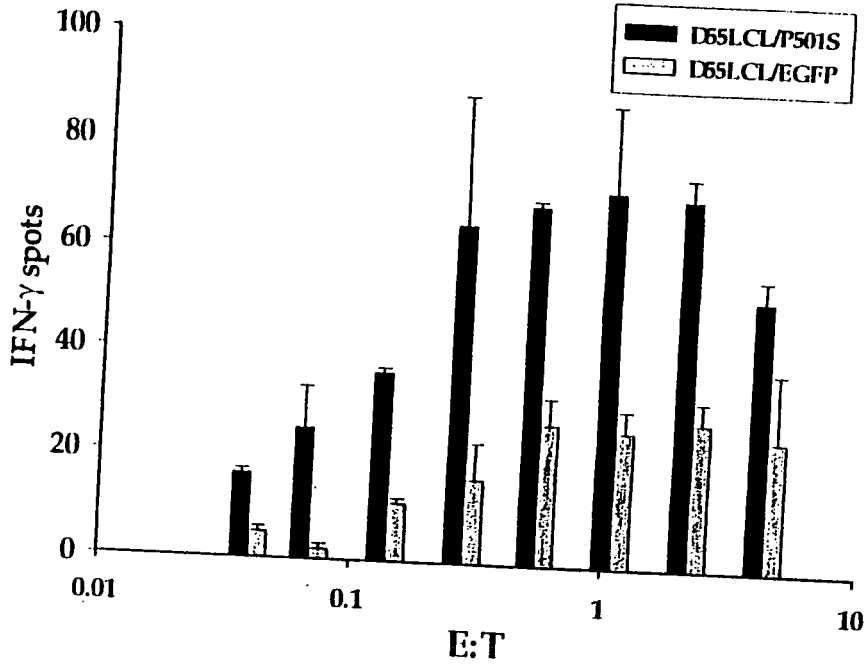
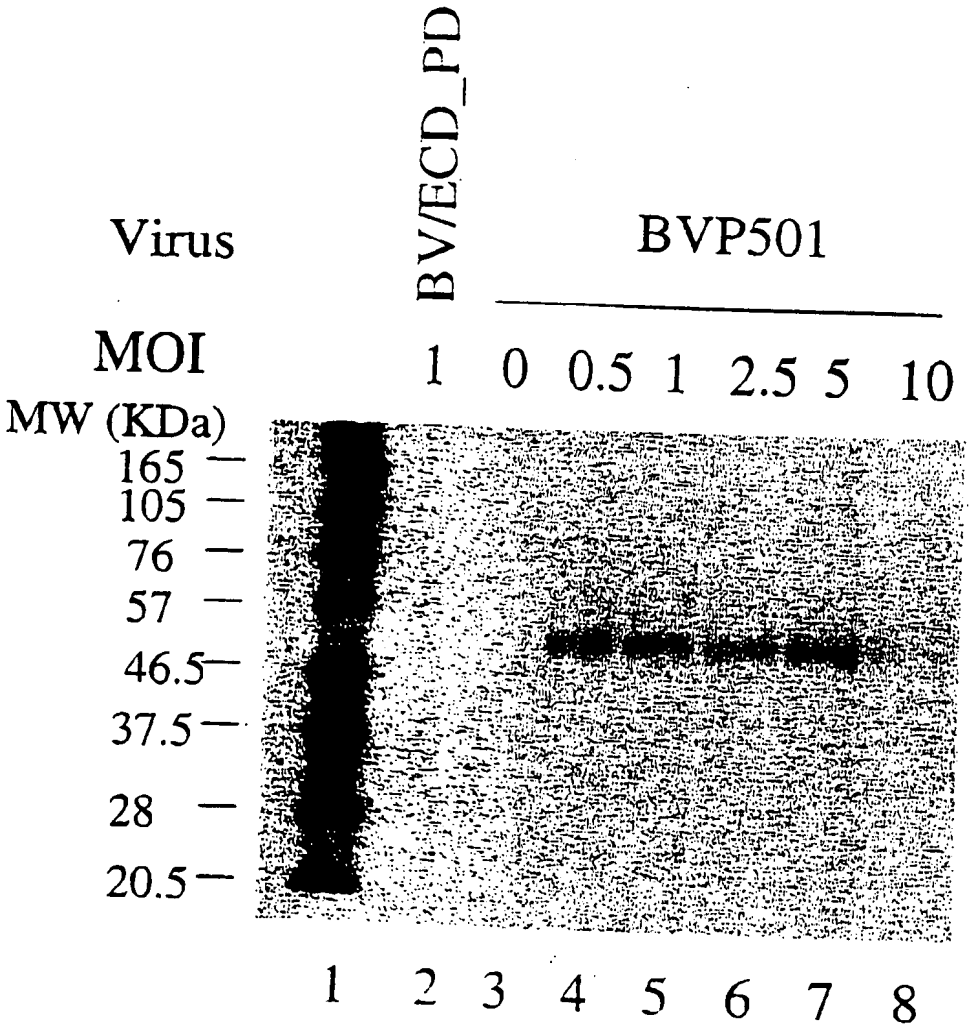


Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 – 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

662TTT' ETE6Eh6D

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

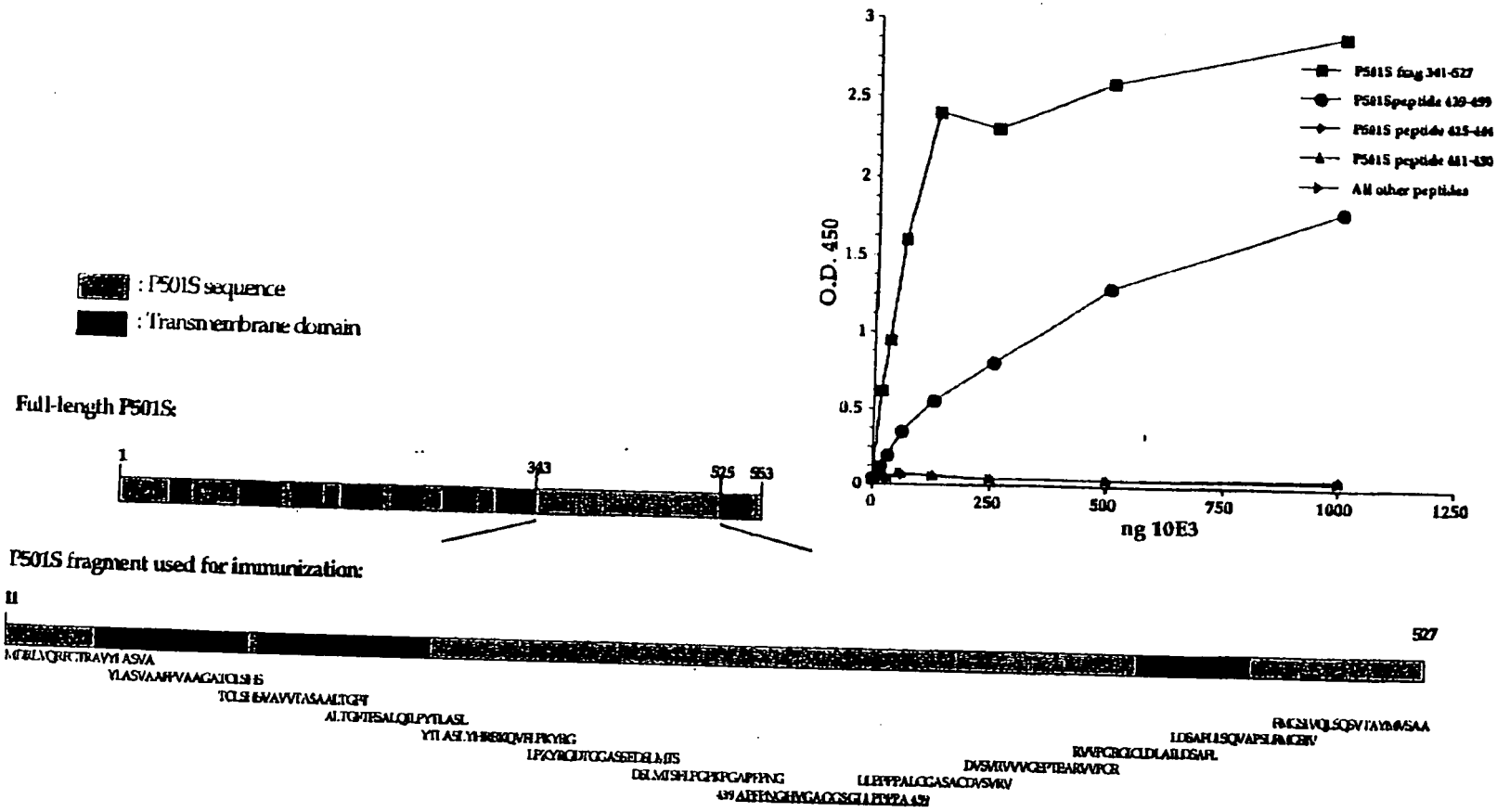


Fig. 8

9062 FF ET66E460

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM TMVLGIGPVLGLVCVPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

FALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWIYTSALAPYLGTQEE

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAEPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA SAA

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

9627TT "ETE5E4bD

Genomic Map of (5) Corixa Candidate Genes

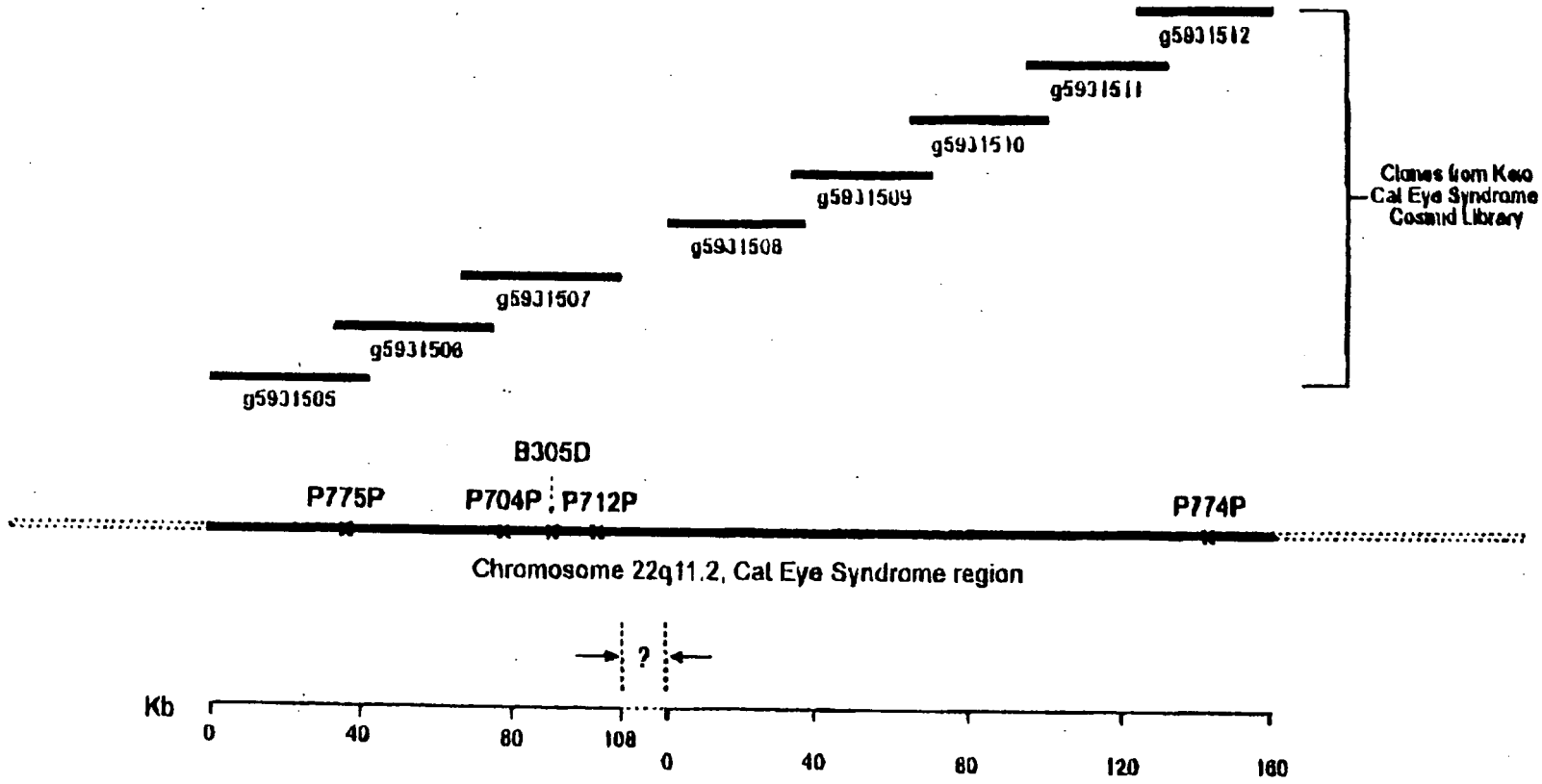


Fig. 10

662TTT"ETE6Eh60

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

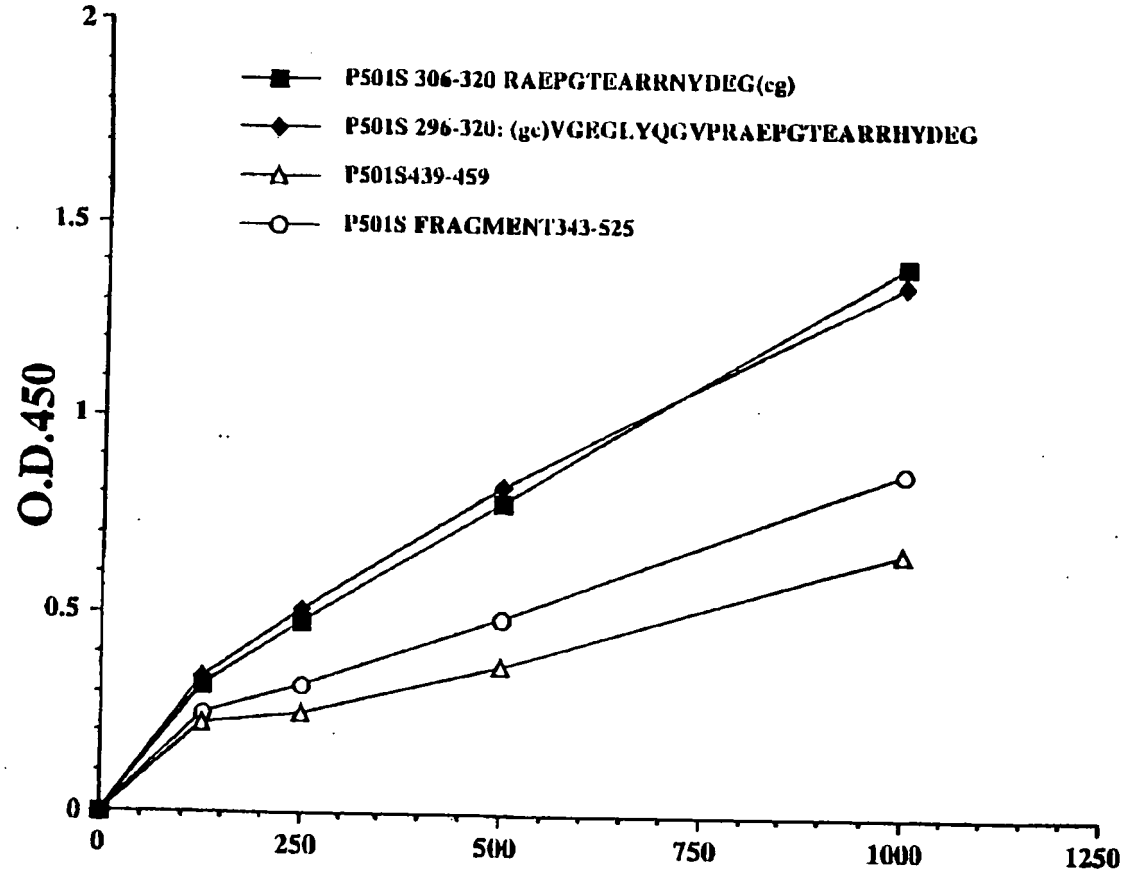


Fig. 11